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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/008,264A

DATE: 11/21/2002

TIME: 20:12:13

Input Set : A:\SEQLIST.txt

Output Set: N:\CRF4\11212002\J008264A.raw

3 <110> APPLICANT: Glimcher, Laurie H.
4 Szabo, Susanne, J.
6 <120> TITLE OF INVENTION: T-BET COMPOSITIONS AND METHODS OF USE THEREOF
8 <130> FILE REFERENCE: HUI-040CP
10 <140> CURRENT APPLICATION NUMBER: US 10/008264A
11 <141> CURRENT FILING DATE: 2001-12-03
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/15345
14 <151> PRIOR FILING DATE: 2000-06-01
16 <150> PRIOR APPLICATION NUMBER: US 60/137085
17 <151> PRIOR FILING DATE: 1999-06-02
19 <160> NUMBER OF SEQ ID NOS: 4
21 <170> SOFTWARE: PatentIn Ver. 2.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1608
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1605)
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37 ccg atg ccg ggg agc gac gag ggc cgg gcg cct ggc gcc gac ccg cag 96
38 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
39 20 25 30
41 cac cgc tac ttc tac ccg gag ccg ggc gcg cag gac gcg gac gag cgt 144
42 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
43 35 40 45
45 cgc ggg ggc ggc agc ctg ggg tct ccc tac ccg ggg ggc gcc ttg gtg 192
46 Arg Gly Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
47 50 55 60
49 ccc gcc ccg ccg agc cgc ttc ctt gga gcc tac gcc tac ccg ccg cga 240
50 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
51 65 70 75 80
53 ccc cag gcg gcc ggc ttc ccc ggc gcg ggc gag tcc ttc ccg ccg ccc 288
54 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
55 85 90 95
57 gcg gac gcc gag ggc tac cag ccg ggc gag ggc tac gcc gcc ccg gac 336
58 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
59 100 105 110
61 ccg cgc gcc ggg ctc tac ccg ggg ccg cgt gag gac tac gcg cta ccc 384
62 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro

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63	115	120	125	
65	gcg gga ctg gag gtg tcg ggg aaa ctg agg gtc gcg ctc aac aac cac	432		
66	Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His			
67	130 135 140			
69	ctg ttg tgg tcc aag ttt aat cag cac cag aca gag atg atc atc acc	480		
70	Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr			
71	145 150 155 160			
73	aag cag gga cgg cgg atg ttc cca ttc ctg tca ttt act gtg gcc ggg	528		
74	Lys Gln Gly Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly			
75	165 170 175			
77	ctg gag ccc acc agc cac tac agg atg ttt gtg gac gtg gtc ttg gtg	576		
78	Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val			
79	180 185 190			
81	gac cag cac cac tgg cgg tac cag agc ggc aag tgg gtg cag tgt gga	624		
82	Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly			
83	195 200 205			
85	aag gcc gag ggc agc atg cca gga aac cgc ctg tac gtc cac ccg gac	672		
86	Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp			
87	210 215 220			
89	tcc ccc aac aca gga gcg cac tgg atg cgc cag gaa gtt tca ttt ggg	720		
90	Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly			
91	225 230 235 240			
93	aaa cta aag ctc aca aac aac aag ggg gcg tcc aac aat gtg acc cag	768		
94	Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln			
95	245 250 255			
97	atg att gtg ctc cag tcc ctc cat aag tac cag ccc cgg ctg cat atc	816		
98	Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile			
99	260 265 270			
101	gtt gag gtg aac gac gga gag cca gag gca gcc tgc aac gct tcc aac	864		
102	Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn			
103	275 280 285			
105	acg cat atc ttt act ttc caa gaa acc cag ttc att gcc gtg act gcc	912		
106	Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala			
107	290 295 300			
109	tac cag aat gcc gag att act cag ctg aaa att gat aat aac ccc ttt	960		
110	Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe			
111	305 310 315 320			
113	gcc aaa gga ttc cgg gag aac ttt gag tcc atg tac aca tct gtt gac	1008		
114	Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp			
115	325 330 335			
117	acc agc atc ccc tcc ccg cct gga ccc aac tgt caa ttc ctt ggg gga	1056		
118	Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly			
119	340 345 350			
121	gat cac tac tct cct ctc cta ccc aac cag tat cct gtt ccc agc cgc	1104		
122	Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg			
123	355 360 365			
125	ttc tac ccc gac ctt cct ggc cag gcg aag gat gtg gtt ccc cag gct	1152		
126	Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala			
127	370 375 380			

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130 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
131 385 390 395 400
133 gca gtc agc atg aag cct gca ttc ttg ccc tct gcc cct ggg ccc acc 1248
134 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
135 405 410 415
137 atg tcc tac tac cga ggc cag gag gtc ctg gca cct gga gct ggc tgg 1296
138 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
139 420 425 430
141 cct gtg gca ccc cag tac cct ccc aag atg ggc ccg gcc agc tgg ttc 1344
142 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
143 435 440 445
145 cgc cct atg cgg act ctg ccc atg gaa ccc ggc cct gga ggc tca gag 1392
146 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
147 450 455 460
149 gga cgg gga cca gag gac cag ggt ccc ccc ttg gtg tgg act gag att 1440
150 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
151 465 470 475 480
153 gcc ccc atc cgg ccg gaa tcc agt gat tca gga ctg ggc gaa gga gac 1488
154 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
155 485 490 495
157 tct aag agg agg cgc gtg tcc ccc tat cct tcc agt ggt gac agc tcc 1536
158 Ser Lys Arg Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser
159 500 505 510
161 tcc cct gct ggg gcc cct tct cct ttt gat aag gaa gct gaa gga cag 1584
162 Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln
163 515 520 525
165 ttt tat aac tat ttt ccc aac tga 1608
166 Phe Tyr Asn Tyr Phe Pro Asn
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172 <212> TYPE: PRT
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179 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
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183 35 40 45
185 Arg Gly Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
186 50 55 60
188 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
189 65 70 75 80
191 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
192 85 90 95
194 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
195 100 105 110
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197 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro
198      115      120      125
200 Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His
201      130      135      140
203 Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr
204 145      150      155      160
206 Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly
207      165      170      175
209 Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val
210      180      185      190
212 Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly
213      195      200      205
215 Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp
216      210      215      220
218 Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly
219 225      230      235      240
221 Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln
222      245      250      255
224 Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile
225      260      265      270
227 Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn
228      275      280      285
230 Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala
231      290      295      300
233 Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe
234 305      310      315      320
236 Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp
237      325      330      335
239 Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly
240      340      345      350
242 Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg
243      355      360      365
245 Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala
246      370      375      380
248 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
249 385      390      395      400
251 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
252      405      410      415
254 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
255      420      425      430
257 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
258      435      440      445
260 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
261      450      455      460
263 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
264 465      470      475      480
266 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
267      485      490      495
269 Ser Lys Arg Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser
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282 <213> ORGANISM: Mus musculus
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286 <222> LOCATION: (1)..(1590)
288 <400> SEQUENCE: 3
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293 ccg atg ccg agt gag gag ggc cgg ggg ccc gga gcg gac caa cag cat 96
294 Pro Met Pro Ser Asp Glu Gly Arg Gly Pro Gly Ala Asp Gln Gln His
295 20 25 30
297 cgt ttc ttc tat ccc gag ccg ggc gca cag gac ccg acc gat cgc cgc 144
298 Arg Phe Phe Tyr Pro Glu Pro Gly Ala Gln Asp Pro Thr Asp Arg Arg
299 35 40 45
301 gca ggt agc agc ctg ggg acg ccc tac tct ggg ggc gcc ctg gtg cct 192
302 Ala Gly Ser Ser Leu Gly Thr Pro Tyr Ser Gly Gly Ala Leu Val Pro
303 50 55 60
305 gcc gcg ccg ggt cgc ttc ctt gga tcc ttc gcc tac ccg ccc cgg gct 240
306 Ala Ala Pro Gly Arg Phe Leu Gly Ser Phe Ala Tyr Pro Pro Arg Ala
307 65 70 75 80
309 cag gtg gct ggc ttt ccc ggg cct ggc gag ttc ttc ccg ccg ccc gcg 288
310 Gln Val Ala Gly Phe Pro Gly Pro Gly Glu Phe Phe Pro Pro Pro Ala
311 85 90 95
313 ggt gcg gag ggc tac ccg ccc gtg gat ggc tac cct gcc cct gac ccg 336
314 Gly Ala Glu Gly Tyr Pro Pro Val Asp Gly Tyr Pro Ala Pro Asp Pro
315 100 105 110
317 cgc gcg ggg ctc tac cca ggg ccg cgc gag gac tac gca ttg ccc gcg 384
318 Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro Ala
319 115 120 125
321 ggg ttg gag gtg tct ggg aag ctg aga gtc gcg ctc agc aac cac ctg 432
322 Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Ser Asn His Leu
323 130 135 140
325 ttg tgg tcc aag ttc aac cag cac cag aca gag atg atc atc act aag 480
326 Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr Lys
327 145 150 155 160
329 caa gga ccg cga atg ttc cca ttc ctg tcc ttc acc gtg gcc ggg ctg 528
330 Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly Leu
331 165 170 175
333 gag ccc aca agc cat tac agg atg ttt gtg gat gtg gtc ttg gtg gac 576
334 Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val Asp
335 180 185 190

VERIFICATION SUMMARY

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